

SEQUENCE LISTING

<110> Mahajan, Pramod B.
Tagliani, Laura

<120> Rad23 Genes and Uses Thereof

<130> 0964D

<150> 09/413,574

<151> 1999-10-06

<150> 60/109,728

<151> 1998-11-23

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<170> FastSEQ for Windows Version 3.0

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<211> 1522

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (58) ... (1272)

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aag ctt aac gtc aag acc ctc aag ggc acc aac ttc gag atc gag gcg	108
Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu Ala	
5 10 15	

agc ccc gat gca tcg gtt gct gat gtg aag agg atc att gag acc act	156
Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr Thr	
20 25 30	

caa ggt cag agt acc tac cgg gcg gac cag caa atg ctc ata tac caa	204
Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr Gln	
35 40 45	

ggg aaa att ctc aag gat gaa acc act ttg gaa agc aac gga gtt gct	252
Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val Ala	
50 55 60 65	

gag aac agc ttc ctt gtt ata atg ttg tcc aag gct aag gca tca tcg	300
Glu Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser Ser	
70 75 80	

agt gga gct tct acc gct act act gca aaa gct cct gca act ctg gcc	348
Ser Gly Ala Ser Thr Ala Thr Thr Ala Lys Ala Pro Ala Thr Leu Ala	
85 90 95	

caa cct gct gcc cct gtg gcc cct gct gca tca gtt gca aga aca cca	396
Gln Pro Ala Ala Pro Val Ala Pro Ala Ala Ser Val Ala Arg Thr Pro	

100	105	110	
aca cag gct cct gtt gcc	aca gct gaa acg gca cct cca agt gtc caa		444
Thr Gln Ala Pro Val Ala	Thr Ala Glu Thr Ala Pro Pro Ser Val Gln		
115	120	125	
cct cag gct gct cca gct gct acg gtt gct gct act gat gat gct gat			492
Pro Gln Ala Ala Pro Ala Ala Thr Val Ala Ala Thr Asp Asp Ala Asp			
130	135	140	145
gtg tac agt cag gca gct tca aac ctt gta ttt ggc aac aat cta gaa			540
Val Tyr Ser Gln Ala Ala Ser Asn Leu Val Phe Gly Asn Asn Leu Glu			
150	155	160	
cag act atc caa caa att ctt gac atg ggt ggt ggt aca tgg gaa cgt			588
Gln Thr Ile Gln Gln Ile Leu Asp Met Gly Gly Gly Thr Trp Glu Arg			
165	170	175	
gat act gtt gtt cgt gct cta cgt gct gca tac aat aac ccc gag aga			636
Asp Thr Val Val Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro Glu Arg			
180	185	190	
gct ata gac tac ctg tat tct gga att cct gag aat gtg gag gct cag			684
Ala Ile Asp Tyr Leu Tyr Ser Gly Ile Pro Glu Asn Val Glu Ala Gln			
195	200	205	
cct gtt gcc cga gca cct gct gct ggc caa caa aca aat cag cag gcc			732
Pro Val Ala Arg Ala Pro Ala Ala Gly Gln Gln Thr Asn Gln Gln Ala			
210	215	220	225
gca tca ccc gct cag cca gca gtt gca ttg cca gtg cag cca tca cct			780
Ala Ser Pro Ala Gln Pro Ala Val Ala Leu Pro Val Gln Pro Ser Pro			
230	235	240	
gcc tct gca ggg cct aat gca aat cct ttg aac ctt ttt cct cag ggt			828
Ala Ser Ala Gly Pro Asn Ala Asn Pro Leu Asn Leu Phe Pro Gln Gly			
245	250	255	
gtt cca agt ggt ggg tcc aac cca ggt gtt gtt cca ggt gca gga tct			876
Val Pro Ser Gly Gly Ser Asn Pro Gly Val Val Pro Gly Ala Gly Ser			
260	265	270	
ggt gct ctt gat gcc ttg cga cag ctt cca cag ttt caa gca ctc ctt			924
Gly Ala Leu Asp Ala Leu Arg Gln Leu Pro Gln Phe Gln Ala Leu Leu			
275	280	285	
cag tta gtc cag gct aat cct caa atc ttg cag cca atg ctt caa gag			972
Gln Leu Val Gln Ala Asn Pro Gln Ile Leu Gln Pro Met Leu Gln Glu			
290	295	300	305
cta ggt aaa caa aac cca caa att ctg cgg ttg att cag gaa aat caa			1020
Leu Gly Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Gln Glu Asn Gln			
310	315	320	
gct gag ttt ctc cgc ttg gtg aat gaa tct cct gag ggt ggt cct gga			1068
Ala Glu Phe Leu Arg Leu Val Asn Glu Ser Pro Glu Gly Gly Pro Gly			
325	330	335	
ggg aac ata cta ggt caa ctg gca gct gct gtg cca caa acg ctg aca			1116
Gly Asn Ile Leu Gly Gln Leu Ala Ala Val Pro Gln Thr Leu Thr			
340	345	350	

gtt acc cca gag gaa cgg gag gct atc cag cgg ctc gag gga atg ggg	1164
Val Thr Pro Glu Glu Arg Glu Ala Ile Gln Arg Leu Glu Gly Met Gly	
355 360 365	
ttc aac cgt gag ctt gtg cta gaa gtt ttc ttt gca tgc aac aag gac	1212
Phe Asn Arg Glu Leu Val Leu Glu Val Phe Phe Ala Cys Asn Lys Asp	
370 375 380 385	
gaa gag ctt aca gcc aac tac ctc ctg gat cat ggc cat gag ttt gac	1260
Glu Glu Leu Thr Ala Asn Tyr Leu Leu Asp His Gly His Glu Phe Asp	
390 395 400	
gat cag cag caa tagacgtggg gtggatggag gaaaccgagg cagttgcaga	1312
Asp Gln Gln	
405	
acagcgagtg tcgttcttat gccctctgcc tgacgagaga tactcggtcg tctatgctat	1372
gctgctgact atcttttatt tccatatata ttgttcgga atgctttcta agtacatatt	1432
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 <213> Zea mays

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35 40 45	
Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val	
50 55 60	
Ala Glu Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser	
65 70 75 80	
Ser Ser Gly Ala Ser Thr Ala Thr Thr Ala Lys Ala Pro Ala Thr Leu	
85 90 95	
Ala Gln Pro Ala Ala Pro Val Ala Pro Ala Ala Ser Val Ala Arg Thr	
100 105 110	
Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Pro Ser Val	
115 120 125	
Gln Pro Gln Ala Ala Pro Ala Ala Thr Val Ala Ala Thr Asp Asp Ala	
130 135 140	
Asp Val Tyr Ser Gln Ala Ala Ser Asn Leu Val Phe Gly Asn Asn Leu	
145 150 155 160	
Glu Gln Thr Ile Gln Gln Ile Leu Asp Met Gly Gly Gly Thr Trp Glu	
165 170 175	
Arg Asp Thr Val Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro Glu	
180 185 190	
Arg Ala Ile Asp Tyr Leu Tyr Ser Gly Ile Pro Glu Asn Val Glu Ala	
195 200 205	
Gln Pro Val Ala Arg Ala Pro Ala Ala Gly Gln Gln Thr Asn Gln Gln	
210 215 220	
Ala Ala Ser Pro Ala Gln Pro Ala Val Ala Leu Pro Val Gln Pro Ser	
225 230 235 240	
Pro Ala Ser Ala Gly Pro Asn Ala Asn Pro Leu Asn Leu Phe Pro Gln	
245 250 255	

Gly Val Pro Ser Gly Gly Ser Asn Pro Gly Val Val Pro Gly Ala Gly
260 265 270

Ser Gly Ala Leu Asp Ala Leu Arg Gln Leu Pro Gln Phe Gln Ala Leu
275 280 285

Leu Gln Leu Val Gln Ala Asn Pro Gln Ile Leu Gln Pro Met Leu Gln
290 295 300

Glu Leu Gly Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Gln Glu Asn
305 310 315 320

Gln Ala Glu Phe Leu Arg Leu Val Asn Glu Ser Pro Glu Gly Gly Pro
325 330 335

Gly Gly Asn Ile Leu Gly Gln Leu Ala Ala Ala Val Pro Gln Thr Leu
340 345 350

Thr Val Thr Pro Glu Glu Arg Glu Ala Ile Gln Arg Leu Glu Gly Met
355 360 365

Gly Phe Asn Arg Glu Leu Val Leu Glu Val Phe Phe Ala Cys Asn Lys
370 375 380

Asp Glu Glu Leu Thr Ala Asn Tyr Leu Leu Asp His Gly His Glu Phe
385 390 395 400

Asp Asp Gln Gln Gln
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<212> DNA
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<220>
<221> CDS
<222> (106)...(1209)

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Met Lys Leu Thr
1

gtg aag acc ctg aag gga acg cac ttc gag atc cgg gtg cag ccc aac 165
Val Lys Thr Leu Lys Gly Thr His Phe Glu Ile Arg Val Gln Pro Asn
5 10 15 20

gac acg att atg gct gtg aag aag aat ata gaa gag ata caa ggg aaa 213
Asp Thr Ile Met Ala Val Lys Lys Asn Ile Glu Glu Ile Gln Gly Lys
25 30 35

gac agc tat cca tgg ggc caa caa ctg ctg att ttc aat gga aag gtc 261
Asp Ser Tyr Pro Trp Gly Gln Gln Leu Leu Ile Phe Asn Gly Lys Val
40 45 50

ttg aaa gat gaa agt aca ttg gaa gag aat aaa gtc aat gag gat ggg 309
Leu Lys Asp Glu Ser Thr Leu Glu Glu Asn Lys Val Asn Glu Asp Gly
55 60 65

ttt cta gtt gtc atg ctt agt aag ggt aaa aca tct ggt tca act gga 357
Phe Leu Val Val Met Leu Ser Lys Gly Lys Thr Ser Gly Ser Thr Gly
70 75 80

act tca tct tcc cag cac tca aac act cct gca aca agg cag gca cct 405
Thr Ser Ser Ser Gln His Ser Asn Thr Pro Ala Thr Arg Gln Ala Pro
85 90 95 100

cct cta gag gcc cca caa caa gct cct caa ccc ccg gtg gca cca att 453

Pro	Leu	Glu	Ala	Pro	Gln	Gln	Ala	Pro	Gln	Pro	Pro	Val	Ala	Pro	Ile	
				105					110					115		
aca	act	tct	cag	cct	gaa	gga	ctt	cct	gca	cag	gca	cct	aac	aca	cat	501
Thr	Thr	Ser	Gln	Pro	Glu	Gly	Leu	Pro	Ala	Gln	Ala	Pro	Asn	Thr	His	
			120					125					130			
gac	aat	gcg	gca	tca	aat	ctt	ctg	tct	gga	agg	aat	gtt	gac	aca	ata	549
Asp	Asn	Ala	Ala	Ser	Asn	Leu	Leu	Ser	Gly	Arg	Asn	Val	Asp	Thr	Ile	
		135				140						145				
att	aac	cag	cta	atg	gag	atg	ggg	ggg	ggc	agt	tgg	gac	aaa	gat	aaa	597
Ile	Asn	Gln	Leu	Met	Glu	Met	Gly	Gly	Gly	Ser	Trp	Asp	Lys	Asp	Lys	
	150					155				160						
gtc	caa	agg	gct	ctc	cgt	gcc	gct	tac	aac	aac	ccc	gaa	cgt	gct	gtt	645
Val	Gln	Arg	Ala	Leu	Arg	Ala	Ala	Tyr	Asn	Asn	Pro	Glu	Arg	Ala	Val	
165					170				175						180	
gaa	tac	ctc	tac	tct	ggg	att	cca	gta	aca	gct	gaa	att	gct	gtt	cca	693
Glu	Tyr	Leu	Tyr	Ser	Gly	Ile	Pro	Val	Thr	Ala	Glu	Ile	Ala	Val	Pro	
				185				190						195		
att	ggg	ggg	caa	ggg	gca	aac	aca	act	gat	cga	gct	cct	act	ggg	gaa	741
Ile	Gly	Gly	Gln	Gly	Ala	Asn	Thr	Thr	Asp	Arg	Ala	Pro	Thr	Gly	Glu	
			200					205					210			
gct	ggg	ctc	tct	ggg	att	cca	aac	acc	gct	cca	cta	gat	ctt	ttc	ccg	789
Ala	Gly	Leu	Ser	Gly	Ile	Pro	Asn	Thr	Ala	Pro	Leu	Asp	Leu	Phe	Pro	
		215					220					225				
cag	ggg	gct	tcc	aat	gct	gga	ggg	ggg	gct	ggg	ggg	gga	cca	ctt	gat	837
Gln	Gly	Ala	Ser	Asn	Ala	Gly	Gly	Gly	Ala	Gly	Gly	Gly	Pro	Leu	Asp	
	230					235					240					
ttt	ctt	aga	aac	aat	cca	cag	ttt	caa	gca	gtt	agg	gaa	atg	gtc	cat	885
Phe	Leu	Arg	Asn	Asn	Pro	Gln	Phe	Gln	Ala	Val	Arg	Glu	Met	Val	His	
245				250					255					260		
aca	aat	cca	caa	att	ttg	cag	cct	atg	ctc	gtt	gag	ttg	agc	aag	cag	933
Thr	Asn	Pro	Gln	Ile	Leu	Gln	Pro	Met	Leu	Val	Glu	Leu	Ser	Lys	Gln	
				265					270					275		
aat	cct	caa	att	cta	agg	ttg	att	gag	gag	aat	cat	gat	gag	ttt	ctt	981
Asn	Pro	Gln	Ile	Leu	Arg	Leu	Ile	Glu	Glu	Asn	His	Asp	Glu	Phe	Leu	
			280					285					290			
cag	tta	cta	aat	gag	ccc	ttt	gaa	ggc	gga	gag	ggg	gat	ttc	tta	gac	1029
Gln	Leu	Leu	Asn	Glu	Pro	Phe	Glu	Gly	Gly	Glu	Gly	Asp	Phe	Leu	Asp	
		295					300					305				
caa	cct	gag	gag	gat	gaa	atg	cct	cat	gcc	att	agt	gtt	aca	cca	gag	1077
Gln	Pro	Glu	Glu	Asp	Glu	Met	Pro	His	Ala	Ile						

gca aac tat ctc ctt gag cat gct ggt gag gaa gat taagcgggag 1219
 Ala Asn Tyr Leu Leu Glu His Ala Gly Glu Glu Asp
 360 365

tagttttcat acgatttttt ttagtaccga gtgacgaaga gttgatatgg agctgacgat 1279
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 gtggtaaaca tcggttctgc tcctgtcctg tattaacaca agcttggtt gggaggaagc 1459
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 aggtgtgcaa gtgtgtaaac gaacgctgcc ttcgtagttc tgacaactgc gacagttctg 1639
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 aaa 1702

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 <212> PRT
 <213> Zea mays

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 20 25 30
 Ile Gln Gly Lys Asp Ser Tyr Pro Trp Gly Gln Gln Leu Leu Ile Phe
 35 40 45
 Asn Gly Lys Val Leu Lys Asp Glu Ser Thr Leu Glu Glu Asn Lys Val
 50 55 60
 Asn Glu Asp Gly Phe Leu Val Val Met Leu Ser Lys Gly Lys Thr Ser
 65 70 75 80
 Gly Ser Thr Gly Thr Ser Ser Ser Gln His Ser Asn Thr Pro Ala Thr
 85 90 95
 Arg Gln Ala Pro Pro Leu Glu Ala Pro Gln Gln Ala Pro Gln Pro Pro
 100 105 110
 Val Ala Pro Ile Thr Thr Ser Gln Pro Glu Gly Leu Pro Ala Gln Ala
 115 120 125
 Pro Asn Thr His Asp Asn Ala Ala Ser Asn Leu Leu Ser Gly Arg Asn
 130 135 140
 Val Asp Thr Ile Ile Asn Gln Leu Met Glu Met Gly Gly Gly Ser Trp
 145 150 155 160
 Asp Lys Asp Lys Val Gln Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro
 165 170 175
 Glu Arg Ala Val Glu Tyr Leu Tyr Ser Gly Ile Pro Val Thr Ala Glu
 180 185 190
 Ile Ala Val Pro Ile Gly Gly Gln Gly Ala Asn Thr Thr Asp Arg Ala
 195 200 205
 Pro Thr Gly Glu Ala Gly Leu Ser Gly Ile Pro Asn Thr Ala Pro Leu
 210 215 220
 Asp Leu Phe Pro Gln Gly Ala Ser Asn Ala Gly Gly Gly Ala Gly Gly
 225 230 235 240
 Gly Pro Leu Asp Phe Leu Arg Asn Asn Pro Gln Phe Gln Ala Val Arg
 245 250 255
 Glu Met Val His Thr Asn Pro Gln Ile Leu Gln Pro Met Leu Val Glu
 260 265 270
 Leu Ser Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Glu Glu Asn His
 275 280 285
 Asp Glu Phe Leu Gln Leu Leu Asn Glu Pro Phe Glu Gly Gly Glu Gly
 290 295 300
 Asp Phe Leu Asp Gln Pro Glu Glu Asp Glu Met Pro His Ala Ile Ser

305					310					315					320
Val	Thr	Pro	Glu	Glu	Gln	Glu	Ala	Ile	Gly	Arg	Leu	Glu	Ser	Met	Gly
				325					330					335	
Phe	Asp	Arg	Ala	Arg	Val	Ile	Glu	Ala	Phe	Leu	Ala	Cys	Asp	Arg	Asn
			340					345					350		
Glu	Glu	Leu	Ala	Ala	Asn	Tyr	Leu	Leu	Glu	His	Ala	Gly	Glu	Glu	Asp
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<210> 5
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

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 tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa
 36